

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/564,585
Source: IFWP
Date Processed by STIC: 1/30/06

ENTERED



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/564,585

DATE: 01/30/2006
TIME: 14:59:12

Input Set : A:\61835-3 SEQ LIST.txt
Output Set: N:\CRF4\01302006\J564585.raw

3 <110> APPLICANT: Vanaja, Donkena Krishna
4 Young, Charles Y.F.
6 <120> TITLE OF INVENTION: Methods And Compositions For Diagnosis, Staging and
Prognosis of

7 Prostate Cancer
9 <130> FILE REFERENCE: 61835-3
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/564,585
C--> 11 <141> CURRENT FILING DATE: 2006-01-13
11 <150> PRIOR APPLICATION NUMBER: US 60/487,553
12 <151> PRIOR FILING DATE: 2003-07-14
14 <150> PRIOR APPLICATION NUMBER: PCT/US2004/022850
15 <151> PRIOR FILING DATE: 2004-07-14

P.6

17 <160> NUMBER OF SEQ ID NOS: 52
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 3614

23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (41)..(1399)

31 <400> SEQUENCE: 1
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33 Met Gln Arg Gln Ala

34 1 5
36 ccc tac aat atc agg cgc agc tct aca tca ggg gac acc gag gag gag 103
37 Pro Tyr Asn Ile Arg Arg Ser Ser Thr Ser Gly Asp Thr Glu Glu Glu

38 10 15 20
40 gag gag gag gtg gtg cca ttc tcc tca gat gaa cag aaa cgg agg 151
41 Glu Glu Glu Val Val Pro Phe Ser Ser Asp Glu Gln Lys Arg Arg

42 25 30 35
44 tca gag gct gca agc ggt gtt ctg agg agg aca gct ccc cgg gag cac 199
45 Ser Glu Ala Ala Ser Gly Val Leu Arg Arg Thr Ala Pro Arg Glu His

46 40 45 50
48 tcc tac gtc ctg tca gcg gcc aag aag agc act ggc agt cct acc cag 247
49 Ser Tyr Val Leu Ser Ala Ala Lys Lys Ser Thr Gly Ser Pro Thr Gln

50 55 60 65
52 gag aca cag gca ccg ttt atc gcg aag agg gtg gag gtg gtg gaa gag 295
53 Glu Thr Gln Ala Pro Phe Ile Ala Lys Arg Val Glu Val Val Glu Glu

54 70 75 80 85
56 gac ggg cct tct gag aag agc cag gac cca cct gct ctg gca aga tcc 343
57 Asp Gly Pro Ser Glu Lys Ser Gln Asp Pro Pro Ala Leu Ala Arg Ser

58 90 95 100
60 act cct ggc tca aac agc tca aga ggt gag gaa att gtc cgc ctg cag

55

103

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61	Thr Pro Gly Ser Asn Ser Ser Arg Gly Glu Glu Ile Val Arg Leu Gln			
62	105	110	115	
64	atc ctg aca ccc agg gca gga ctc cgc ctg gtg gcc cca gac gtg gaa		439	
65	Ile Leu Thr Pro Arg Ala Gly Leu Arg Leu Val Ala Pro Asp Val Glu			
66	120	125	130	
68	ggc atg agc tcc agt gcc act tca gtc tct gct gtc cct gct gat agg		487	
69	Gly Met Ser Ser Ala Thr Ser Val Ser Ala Val Pro Ala Asp Arg			
70	135	140	145	
72	aag agc aac agc aca gca gcc cag gag gat gca aag gca gac cca aag		535	
73	Lys Ser Asn Ser Thr Ala Ala Gln Glu Asp Ala Lys Ala Asp Pro Lys			
74	150	155	160	165
76	ggg gcc ttg gct gat tgt gag ggg aag gat gta ccc acc agg gtc gga		583	
77	Gly Ala Leu Ala Asp Cys Glu Gly Lys Asp Val Pro Thr Arg Val Gly			
78	170	175	180	
80	gag gcc tgg cag gag agg cct gga gct cca aga ggt ggc caa gga gac		631	
81	Glu Ala Trp Gln Glu Arg Pro Gly Ala Pro Arg Gly Gln Gly Asp			
82	185	190	195	
84	cca gct gta ccc gct cag caa cct gca gat ccc agc acc cca gag cgg		679	
85	Pro Ala Val Pro Ala Gln Gln Pro Ala Asp Pro Ser Thr Pro Glu Arg			
86	200	205	210	
88	cag agc agc ccc agc gga tct gag caa ctt gtc aga cga gag agt tgt		727	
89	Gln Ser Ser Pro Ser Gly Ser Glu Gln Leu Val Arg Arg Glu Ser Cys			
90	215	220	225	
92	ggc agt agc gtg ttg act gat ttt gag ggg aag gat gtg gcc acc aag		775	
93	Gly Ser Ser Val Leu Thr Asp Phe Glu Gly Lys Asp Val Ala Thr Lys			
94	230	235	240	245
96	gtc gga gag gcc tgg cag gac agg cct aga gcc cca aga ggt ggc caa		823	
97	Val Gly Glu Ala Trp Gln Asp Arg Pro Arg Ala Pro Arg Gly Gln			
98	250	255	260	
100	gga gac cca gct gta ccc act cag caa cct gca gat ccc agt acc cca		871	
101	Gly Asp Pro Ala Val Pro Thr Gln Gln Pro Ala Asp Pro Ser Thr Pro			
102	265	270	275	
104	gaa cag cag aac agc ccc agc gga tct gag caa ttc gtc aga cga gag		919	
105	Glu Gln Asn Ser Pro Ser Gly Ser Glu Gln Phe Val Arg Arg Glu			
106	280	285	290	
108	agc tgc acc agc agg gtg agg agc ccc tcg agc tgc atg gtc act gtt		967	
109	Ser Cys Thr Ser Arg Val Arg Ser Pro Ser Ser Cys Met Val Thr Val			
110	295	300	305	
112	act gtc act gcc aca tct gag cag cct cac att tat att cca gcc ccc		1015	
113	Thr Val Thr Ala Thr Ser Glu Gln Pro His Ile Tyr Ile Pro Ala Pro			
114	310	315	320	325
116	gca agt gaa ttg gac tcc agc tct acc acc aaa ggg att ctc ttc gtg		1063	
117	Ala Ser Glu Leu Asp Ser Ser Ser Thr Thr Lys Gly Ile Leu Phe Val			
118	330	335	340	
120	aag gag tac gtg aat gct agt gaa gtg tct tct ggg aag cca gta tct		1111	
121	Lys Glu Tyr Val Asn Ala Ser Glu Val Ser Ser Gly Lys Pro Val Ser			
122	345	350	355	
124	gca cgc tat agc aac gtc agc agc att gag gac tca ttc gcc atg gag		1159	
125	Ala Arg Tyr Ser Asn Val Ser Ser Ile Glu Asp Ser Phe Ala Met Glu			

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126	360	365	370	
128	aag aag cct cca tgt ggc agc act cca tac tct gag agg aca act gga			1207
129	Lys Lys Pro Pro Cys Gly Ser Thr Pro Tyr Ser Glu Arg Thr Thr Gly			
130	375	380	385	
132	ggg atc tgt act tac tgc aac cgt gag atc cga gac tgt cca aag att			1255
133	Gly Ile Cys Thr Tyr Cys Asn Arg Glu Ile Arg Asp Cys Pro Lys Ile			
134	390	395	400	405
136	acc cta gaa cat ctt ggt atc tgc tgc cat gaa tat tgc ttt aag tgt			1303
137	Thr Leu Glu His Leu Gly Ile Cys Cys His Glu Tyr Cys Phe Lys Cys			
138	410	415	420	
140	ggg att tgc agt aaa ccg atg ggc gat ctc ctg gat cag atc ttc att			1351
141	Gly Ile Cys Ser Lys Pro Met Gly Asp Leu Leu Asp Gln Ile Phe Ile			
142	425	430	435	
144	cac cgt gac acc att cac tgt ggg aaa tgc tat gag aag ctc ttc tag			1399
145	His Arg Asp Thr Ile His Cys Gly Lys Cys Tyr Glu Lys Leu Phe			
146	440	445	450	
148	cgaccccca ccggcaggct gatcagaagc tgatgactcg tggacaaatt tggctgtccc			1459
150	cagtttgcc ccaagttgct gtctccctt ccctcacctc ctccctccct gtttgatttc			1519
152	ttcatgcttt tgcccttctc aagttgaagt tgcatacacatc caatatcgta tcttaatgat			1579
154	gctatgataa ttgcttgtgt gtgttagcttc ttgttagctta gaaagcgcctt tatgcccattg			1639
156	atgtcatttc aggctcaacc aaagaggatc aaacaggaat tccatcttgg ctccctaag			1699
158	acagattggc ttctaatga gtttaagtgg gcagaagtgtt agggttcagt gtgtcctgac			1759
160	tcccttgagg cttataatgg gccaagttga agactgtga tgatccctgg tggtaaatt			1819
162	gcagacatca aatgctaggg attggcatag gctagtgttt agcttgcata tttgccccat			1879
164	ctatttttt aaatttccat acacttgtaa aagtagttag ttgctttga tttagttata			1939
166	tagcagttt tcattttggc ttccactcac cgttcactat atttgagttt tcccttacag			1999
168	gtatgttggc atgtgttggaa aattttacac aatttaggtt aaattcagta ggatgtgatt			2059
170	ttgggggtgg actgatcaaa gtgatatatcg tgcgtgttgg aatcttgata gctgattaat			2119
172	ttgcctcaa ttctgctccc tgaacttcac acataaaatct tcccaagtgg gttttaggg			2179
174	gtatagatcc cagcaggatt aaggaagtgg aaaagcagct aacatttctt gaggtctac			2239
176	cacatagcag gcactgtcac agagtaatgg cattaatccc cataataatc ctgtgaaggt			2299
178	gatattctca tcccattta gacatgagga tatttggact cagagagggt gctattgcat			2359
180	tgcgcagaac gctacagagc ccatgcttt cccagagcag caccacaaa agcaagcatt			2419
182	gattttgtgc tcagtgtgt ccaagcactg tgccaggggt acacagtcc tgccaggtt			2479
184	acaccctccc ttcaaggcctc ccaaaggcat aggcttgcac agagcagaag gtgtgaaatc			2539
186	acactcttcc tctggccatc ctggatccct gaattatccc ccccccattg aagtaacttca			2599
188	agggccaagc tgcccttcc cctcccttcc gcccattaaa atgcctccaa actgagatgc			2659
190	tttcagctga gaacagattt gactcacaga cattacaaa gaggagctt tgaatccagg			2719
192	aaaagctcca gggggctagc tgatctgagc agagagctt cagtgcacca tttcctgtc			2779
194	tagactctgc cttaaagcttag tggcaactgc tggggccca ggtacttggg acatggaaac			2839
196	tcgttggatg gctggcaga tgcataaggctt cccatgcagt cagccgatcc tctgctcagg			2899
198	ttcagctgga ctctggccatc tggggccca gcatcactct gtaagttct tggaaagggaa			2959
200	aacaacctta gatgtttt gataaaaaat gaggccctt gctttgatt taattataaa			3019
202	atgtctacgt ctttctccag ttctgagcc ccatgcacat tggcttgg gcttggctt			3079
204	cctgccaaat gatcagagag ggaacattcc atttatttgc agtggattc ctctggagg			3139
206	catgtaccca cactaaatac caactgcttc tcctcagctg tagtccccaa catcagactt			3199
208	ggcacgttgt ggacactaac acacaggcac tcaatgaatg agtgaaggaa ataaaaagtca			3259
210	ccccccgttg gtgagaaggt gcctatcccc ctgagtcctc agtgcaggac cagtgatgt			3319
212	aaggcaaggt aaagaggccc aaagataggct ggcttcccccc gttcaaggtt tagtctgcct			3379

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214 ttaaggagt tttagaacca acatgcaaga cattgaaaga aatcttgcaa gagccattat 3439
 216 tgacttagat ccaaaacagc ctctctcatg tctaaaaagg cacagaattt tgcagatctg 3499
 218 aggaagaggg atgcattacc ttttgcttc ttttcaattt ctttagtgtt ctaatcatac 3559
 220 ttaatccaca ctaatgtcg caattataat aaatgctaaa atatcaaaaa aaaaa 3614
 223 <210> SEQ ID NO: 2
 224 <211> LENGTH: 452
 225 <212> TYPE: PRT
 226 <213> ORGANISM: Homo sapiens
 228 <400> SEQUENCE: 2
 230 Met Gln Arg Gln Ala Pro Tyr Asn Ile Arg Arg Ser Ser Thr Ser Gly
 231 1 5 10 15
 234 Asp Thr Glu Glu Glu Glu Glu Val Val Pro Phe Ser Ser Asp
 235 20 25 30
 238 Glu Gln Lys Arg Arg Ser Glu Ala Ala Ser Gly Val Leu Arg Arg Thr
 239 35 40 45
 242 Ala Pro Arg Glu His Ser Tyr Val Leu Ser Ala Ala Lys Lys Ser Thr
 243 50 55 60
 246 Gly Ser Pro Thr Gln Glu Thr Gln Ala Pro Phe Ile Ala Lys Arg Val
 247 65 70 75 80
 250 Glu Val Val Glu Glu Asp Gly Pro Ser Glu Lys Ser Gln Asp Pro Pro
 251 85 90 95
 254 Ala Leu Ala Arg Ser Thr Pro Gly Ser Asn Ser Ser Arg Gly Glu Glu
 255 100 105 110
 258 Ile Val Arg Leu Gln Ile Leu Thr Pro Arg Ala Gly Leu Arg Leu Val
 259 115 120 125
 262 Ala Pro Asp Val Glu Gly Met Ser Ser Ser Ala Thr Ser Val Ser Ala
 263 130 135 140
 266 Val Pro Ala Asp Arg Lys Ser Asn Ser Thr Ala Ala Gln Glu Asp Ala
 267 145 150 155 160
 270 Lys Ala Asp Pro Lys Gly Ala Leu Ala Asp Cys Glu Gly Lys Asp Val
 271 165 170 175
 274 Pro Thr Arg Val Gly Glu Ala Trp Gln Glu Arg Pro Gly Ala Pro Arg
 275 180 185 190
 278 Gly Gly Gln Gly Asp Pro Ala Val Pro Ala Gln Gln Pro Ala Asp Pro
 279 195 200 205
 282 Ser Thr Pro Glu Arg Gln Ser Ser Pro Ser Gly Ser Glu Gln Leu Val
 283 210 215 220
 286 Arg Arg Glu Ser Cys Gly Ser Ser Val Leu Thr Asp Phe Glu Gly Lys
 287 225 230 235 240
 290 Asp Val Ala Thr Lys Val Gly Glu Ala Trp Gln Asp Arg Pro Arg Ala
 291 245 250 255
 294 Pro Arg Gly Gly Gln Gly Asp Pro Ala Val Pro Thr Gln Gln Pro Ala
 295 260 265 270
 298 Asp Pro Ser Thr Pro Glu Gln Gln Asn Ser Pro Ser Gly Ser Glu Gln
 299 275 280 285
 302 Phe Val Arg Arg Glu Ser Cys Thr Ser Arg Val Arg Ser Pro Ser Ser
 303 290 295 300
 306 Cys Met Val Thr Val Thr Val Thr Ala Thr Ser Glu Gln Pro His Ile
 307 305 310 315 320

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310 Tyr Ile Pro Ala Pro Ala Ser Glu Leu Asp Ser Ser Ser Thr Thr Lys
 311 325 330 335
 314 Gly Ile Leu Phe Val Lys Glu Tyr Val Asn Ala Ser Glu Val Ser Ser
 315 340 345 350
 318 Gly Lys Pro Val Ser Ala Arg Tyr Ser Asn Val Ser Ser Ile Glu Asp
 319 355 360 365
 322 Ser Phe Ala Met Glu Lys Lys Pro Pro Cys Gly Ser Thr Pro Tyr Ser
 323 370 375 380
 326 Glu Arg Thr Thr Gly Gly Ile Cys Thr Tyr Cys Asn Arg Glu Ile Arg
 327 385 390 395 400
 330 Asp Cys Pro Lys Ile Thr Leu Glu His Leu Gly Ile Cys Cys His Glu
 331 405 410 415
 334 Tyr Cys Phe Lys Cys Gly Ile Cys Ser Lys Pro Met Gly Asp Leu Leu
 335 420 425 430
 338 Asp Gln Ile Phe Ile His Arg Asp Thr Ile His Cys Gly Lys Cys Tyr
 339 435 440 445
 342 Glu Lys Leu Phe
 343 450
 346 <210> SEQ ID NO: 3
 347 <211> LENGTH: 23
 348 <212> TYPE: DNA
 349 <213> ORGANISM: artificial sequence
 351 <220> FEATURE:
 352 <223> OTHER INFORMATION: ZNF 185 forward primer
 354 <400> SEQUENCE: 3
 355 tggatgaaag gcaaggtaaa gag 23
 358 <210> SEQ ID NO: 4
 359 <211> LENGTH: 26
 360 <212> TYPE: DNA
 361 <213> ORGANISM: artificial sequence
 363 <220> FEATURE:
 364 <223> OTHER INFORMATION: ZNF 185 reverse primer
 366 <400> SEQUENCE: 4
 367 ttctaaaact cccttaaagg cagact 26
 370 <210> SEQ ID NO: 5
 371 <211> LENGTH: 23
 372 <212> TYPE: DNA
 373 <213> ORGANISM: artificial sequence
 375 <220> FEATURE:
 376 <223> OTHER INFORMATION: ZNF 185 probe
 378 <400> SEQUENCE: 5
 379 ccaagatagg ctggcttccc ccg 23
 382 <210> SEQ ID NO: 6
 383 <211> LENGTH: 30
 384 <212> TYPE: DNA
 385 <213> ORGANISM: artificial sequence
 387 <220> FEATURE:
 388 <223> OTHER INFORMATION: PSP94 forward primer
 390 <400> SEQUENCE: 6

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/30/2006
PATENT APPLICATION: US/10/564,585 TIME: 14:59:13

Input Set : A:\61835-3 SEQ LIST.txt
Output Set: N:\CRF4\01302006\J564585.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:37; N Pos. 505

VERIFICATION SUMMARY

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Input Set : A:\61835-3 SEQ LIST.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:480